

RAW SEQUENCE LISTING

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Application Serial Number: 10/501, 098

Source: IFWO

Date Processed by STIC: 06/24/2005

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IFWO

RAW SEQUENCE LISTING

DATE: 06/24/2005

PATENT APPLICATION: US/10/501,098

TIME: 11:27:04

Input Set : A:\4121-169.ST25.txt

Output Set: N:\CRF4\06242005\J501098.raw

3 <110> APPLICANT: Petzelt, Christian
 5 <120> TITLE OF INVENTION: Cytotoxic Cyplasin of the Sea Hare, Aplysia Punctata, cDNA
 7 <130> FILE REFERENCE: 4121-169
 9 <140> CURRENT APPLICATION NUMBER: 10/501,098
 C--> 10 <141> CURRENT FILING DATE: 2004-07-07
 12 <150> PRIOR APPLICATION NUMBER: PCT/EP02/14511
 13 <151> PRIOR FILING DATE: 2002-12-18
 15 <160> NUMBER OF SEQ ID NOS: 5
 17 <170> SOFTWARE: PatentIn version 3.3
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 558
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Aplysia punctata
 24 <400> SEQUENCE: 1
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 30 Val Ser Gly Arg Thr Val Cys Glu Ser Lys Gln Glu Cys Asp Ala Ala
 31 20 25 30
 34 Gln Cys Asp Lys Thr Leu Asp Val Ala Ile Val Gly Ala Gly Ala Ala
 35 35 40 45
 38 Gly Ala Tyr Ser Ala Tyr Leu Leu Arg Asn Lys Gly Gln Asn Ile Gly
 39 50 55 60
 42 Val Phe Glu Phe Cys Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln
 43 65 70 75 80
 46 Leu Pro Asn Thr Pro Asp Val Gln Leu Glu Leu Gly Gly Met Arg Tyr
 47 85 90 95
 50 Ile Thr Gly Ala His Asn Leu Leu Glu Gly Val Val Arg Gln Leu Gly
 51 100 105 110
 54 Leu Thr Pro Val Val Phe Thr Glu Gly Phe Gly Lys Leu Gly Arg Thr
 55 115 120 125
 58 Arg Tyr Tyr Leu Arg Gly Gln Ser Leu Thr Phe Gln Glu Val Leu Thr
 59 130 135 140
 62 Gly Asp Val Pro Tyr Asn Leu Thr Val Ala Glu Lys Gln Asn Gln Asp
 63 145 150 155 160
 66 Asn Ile Phe Ala Phe Tyr Leu Lys Glu Leu Thr Arg Phe Asp Val Gly
 67 165 170 175
 70 Asp Gly Phe Val Thr Arg Glu Gln Leu Leu Lys Leu Arg Val Ser Asp
 71 180 185 190
 74 Gly Arg Leu Leu Tyr Gln Leu Thr Phe Asp Glu Ala Leu Asp Leu Val
 75 195 200 205
 78 Ala Ser Pro Glu Gly Lys Glu Phe Ala Arg Asp Ile His Val Phe Thr
 79 210 215 220
 82 Thr Glu Val Ser Asp Asp Ala Asn Ala Val Ser Val Phe Asp Asp His

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86 Leu Gly Glu Asp Gly Val Gly Glu Glu Ile His Thr Val Gln Glu Gly
87          245          250          255
90 Met Gln Lys Val Pro Glu Gln Leu Leu Arg Ala Phe Gly Asn Ser Ser
91          260          265          270
94 Val Phe Gly His Arg Val Phe Thr Asn Leu Gln Leu Lys Ala Ile Arg
95          275          280          285
98 Ser Lys Ser Asp Lys Ser His Val Leu Tyr Phe Arg Thr Thr Ser Thr
99          290          295          300
102 Val Asp Gly Lys Thr Thr Ile Leu Lys Phe Glu Pro Leu Gln Lys Val
103 305          310          315          320
106 Cys Thr Arg Gln Ile Ile Leu Ala Leu Pro Val Phe Ala Leu Met Gln
107          325          330          335
110 Val Asp Trp Pro Pro Leu Arg Glu Asn Arg Ala Gln Lys Ala Tyr Gly
111          340          345          350
114 Ala Val Arg Thr Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln
115          355          360          365
118 Pro Trp Trp Leu Gln Asn Asp Val Thr Asp Phe Pro Ala Phe Val Thr
119          370          375          380
122 Lys Gly Asp Thr Thr Phe Ser Gln Met Tyr Asp Trp Lys Lys Ser Glu
123 385          390          395          400
126 Ala Ser Gly Asp Tyr Ile Leu Ile Ala Ser Tyr Ala Asp Gly Asn Asn
127          405          410          415
130 Thr Leu Phe Gln Arg Val Leu Arg Asp Gln Gly Glu Pro Ile Asn Gly
131          420          425          430
134 Ser Glu Ala Gly Ala His Ile Val Ser Glu Pro Leu Lys Asn Gln Ile
135          435          440          445
138 Leu Asp His Leu Ala Asp Ala Phe Gly Val Pro Arg Ser Asp Ile Gln
139          450          455          460
142 Glu Pro Lys Thr Ala Val Ser Lys Phe Trp Thr Asp Tyr Pro Phe Gly
143 465          470          475          480
146 Cys Gly Trp Ile Thr Trp Arg Ala Gly Tyr His Phe Asp Asp Val Met
147          485          490          495
150 Asn Thr Met Arg Arg Pro Ser Leu Thr Asp Glu Val Tyr Val Val Gly
151          500          505          510
154 Ala Asp Tyr Ser Trp Gly Leu Ile Ser Ser Trp Val Glu Gly Ala Leu
155          515          520          525
158 Glu Thr Ser Tyr Glu Val Ile Asp Thr Tyr Phe Lys Ser Glu Arg Ser
159          530          535          540
162 His Asn Val Gln Pro Pro Ser His Met Ala Ser His Val Gly
163 545          550          555
166 <210> SEQ ID NO: 2
167 <211> LENGTH: 421
168 <212> TYPE: PRT
169 <213> ORGANISM: Aplysia punctata
171 <400> SEQUENCE: 2
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177 Val Ser Gly Arg Thr Val Cys Glu Ser Lys Gln Glu Cys Asp Ala Ala

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178          20          25          30
181 Gln Cys Asp Lys Thr Leu Asp Val Ala Ile Val Gly Ala Gly Ala Ala
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185 Gly Ala Tyr Ser Ala Tyr Leu Leu Arg Asn Lys Gly Gln Asn Ile Gly
186          50          55          60
189 Val Phe Glu Phe Cys Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln
190 65          70          75          80
193 Leu Pro Asn Thr Pro Asp Val Gln Leu Glu Leu Gly Gly Met Arg Tyr
194          85          90          95
197 Ile Thr Gly Ala His Asn Leu Leu Glu Gly Val Val Arg Gln Leu Gly
198          100         105         110
201 Leu Thr Pro Val Val Phe Thr Glu Gly Phe Gly Lys Leu Gly Arg Thr
202          115         120         125
205 Arg Tyr Tyr Pro Arg Gly Gln Ser Leu Thr Phe Gln Glu Ala Leu Thr
206          130         135         140
209 Gly Asp Val Pro Tyr Asn Leu Thr Val Ala Glu Lys Gln Asn Gln Asp
210 145          150         155         160
213 Asn Ile Phe Ala Phe Tyr Leu Lys Glu Leu Thr Arg Phe Asp Val Gly
214          165         170         175
217 Asp Gly Phe Val Thr Arg Glu Gln Leu Leu Lys Leu Arg Ala Ser Asp
218          180         185         190
221 Gly Arg Pro Leu Tyr Gln Leu Thr Phe Asp Glu Ala Leu Asp Leu Val
222          195         200         205
225 Ala Ser Pro Glu Gly Lys Glu Phe Ala Arg Asp Ile His Val Phe Thr
226          210         215         220
229 Thr Glu Val Ser Asp Asp Ala Asn Ala Val Ser Val Phe Asp Asp His
230 225          230         235         240
233 Leu Gly Glu Asp Gly Val Gly Glu Glu Ile His Thr Val Gln Glu Gly
234          245         250         255
237 Met Gln Lys Val Pro Glu Gln Pro Leu Arg Ala Phe Gly Asn Ser Ser
238          260         265         270
241 Val Phe Gly His Arg Val Phe Thr Asn Leu Gln Leu Lys Ala Ile Arg
242          275         280         285
245 Ala Lys Ser Asp Lys Ser His Val Pro Tyr Phe Arg Pro Thr Ser Thr
246          290         295         300
249 Val Asp Gly Lys Thr Thr Ile Leu Lys Phe Glu Pro Leu Gln Lys Val
250 305          310         315         320
253 Cys Ala Arg Gln Ile Ile Leu Ala Leu Pro Val Phe Ala Leu Met Gln
254          325         330         335
257 Val Asp Trp Pro Pro Leu Arg Glu Asn Arg Ala Gln Lys Ala Tyr Gly
258          340         345         350
261 Ala Val Arg Thr Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln
262          355         360         365
265 Pro Trp Trp Leu Gln Asn Asp Val Thr Asp Phe Pro Ala Phe Val Thr
266          370         375         380
269 Lys Gly Asp Thr Thr Phe Ser Gln Met Tyr Asp Trp Lys Lys Pro Asn
270 385          390         395         400
273 Val Ser Gly Asp Tyr Ile Leu Ile Ala Ser Tyr Ala Asp Gly Ser Thr
274          405         410         415

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278          420
281 <210> SEQ ID NO: 3
282 <211> LENGTH: 506
283 <212> TYPE: PRT
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: Synthetic Construct
289 <400> SEQUENCE: 3
291 Ala Tyr Leu Leu Arg Asn Lys Gly Gln Asn Ile Gly Val Phe Glu Phe
292 1          5          10          15
295 Cys Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro Asn Thr
296          20          25          30
299 Pro Asp Val Gln Leu Glu Leu Gly Met Arg Tyr Ile Thr Gly Ala
300          35          40          45
303 His Asn Leu Leu Glu Gly Val Val Arg Gln Leu Gly Leu Thr Pro Val
304          50          55          60
307 Val Phe Thr Glu Gly Phe Gly Lys Leu Gly Arg Thr Arg Tyr Tyr Leu
308 65          70          75          80
311 Arg Gly Gln Ser Leu Thr Phe Gln Glu Val Leu Thr Gly Asp Val Pro
312          85          90          95
315 Tyr Asn Leu Thr Val Ala Glu Lys Gln Asn Gln Asp Asn Ile Phe Ala
316          100         105         110
319 Phe Tyr Leu Lys Glu Leu Thr Arg Phe Asp Val Gly Asp Gly Phe Val
320          115         120         125
323 Thr Arg Glu Gln Leu Leu Lys Leu Arg Val Ser Asp Gly Arg Leu Leu
324          130         135         140
327 Tyr Gln Leu Thr Phe Asp Glu Ala Leu Asp Leu Val Ala Ser Pro Glu
328 145         150         155         160
331 Gly Lys Glu Phe Ala Arg Asp Ile His Val Phe Thr Thr Glu Val Ser
332          165         170         175
335 Asp Asp Ala Asn Ala Val Ser Val Phe Asp Asp His Leu Gly Glu Asp
336          180         185         190
339 Gly Val Gly Glu Glu Ile His Thr Val Gln Glu Gly Met Gln Lys Val
340          195         200         205
343 Pro Glu Gln Leu Leu Arg Ala Phe Gly Asn Ser Ser Val Phe Gly His
344          210         215         220
347 Arg Val Phe Thr Asn Leu Gln Leu Lys Ala Ile Arg Ser Lys Ser Asp
348 225         230         235         240
351 Lys Ser His Val Leu Tyr Phe Arg Thr Thr Ser Thr Val Asp Gly Lys
352          245         250         255
355 Thr Thr Ile Leu Lys Phe Glu Pro Leu Gln Lys Val Cys Thr Arg Gln
356          260         265         270
359 Ile Ile Leu Ala Leu Pro Val Phe Ala Leu Met Gln Val Asp Trp Pro
360          275         280         285
363 Pro Leu Arg Glu Asn Arg Ala Gln Lys Ala Tyr Gly Ala Val Arg Thr
364          290         295         300
367 Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp Leu
368 305         310         315         320

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371 Gln Asn Asp Val Thr Asp Phe Pro Ala Phe Val Thr Lys Gly Asp Thr
372           325           330           335
375 Thr Phe Ser Gln Met Tyr Asp Trp Lys Lys Ser Glu Ala Ser Gly Asp
376           340           345           350
379 Tyr Ile Leu Ile Ala Ser Tyr Ala Asp Gly Asn Asn Thr Leu Phe Gln
380           355           360           365
383 Arg Val Leu Arg Asp Gln Gly Glu Pro Ile Asn Gly Ser Glu Ala Gly
384           370           375           380
387 Ala His Ile Val Ser Glu Pro Leu Lys Asn Gln Ile Leu Asp His Leu
388 385           390           395           400
391 Ala Asp Ala Phe Gly Val Pro Arg Ser Asp Ile Gln Glu Pro Lys Thr
392           405           410           415
395 Ala Val Ser Lys Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile
396           420           425           430
399 Thr Trp Arg Ala Gly Tyr His Phe Asp Asp Val Met Asn Thr Met Arg
400           435           440           445
403 Arg Pro Ser Leu Thr Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser
404           450           455           460
407 Trp Gly Leu Ile Ser Ser Trp Val Glu Gly Ala Leu Glu Thr Ser Tyr
408 465           470           475           480
411 Glu Val Ile Asp Thr Tyr Phe Lys Ser Glu Arg Ser His Asn Val Gln
412           485           490           495
415 Pro Pro Ser His Met Ala Ser His Val Gly
416           500           505

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419 <210> SEQ ID NO: 4

420 <211> LENGTH: 12

421 <212> TYPE: PRT

422 <213> ORGANISM: Artificial Sequence

424 <220> FEATURE:

425 <223> OTHER INFORMATION: Synthetic construct

427 <400> SEQUENCE: 4

429 Ser Gly Asp Tyr Ile Leu Ile Ala Ser Tyr Ala Asp

430 1 5 10

433 <210> SEQ ID NO: 5

434 <211> LENGTH: 1518

435 <212> TYPE: DNA

436 <213> ORGANISM: Aplysia punctata

438 <400> SEQUENCE: 5

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441 ggtggtcggc tgttcaccta tcagttgcct aatacccccg acgtgcagct ggaactgggc      120
443 gggatgcggg acatcaccgg cgctcataac ctgctcgagg gagtcgttcg tcagctggga      180
445 ctgaccccag tagtgtttac agaaggcttc ggtaagctgg gccgtacacg ctattacctg      240
447 aggggacagt ccctgacctt ccaggaagtg ctgacaggcg acgtgccata caaccttacc      300
449 gtcgcggaga agcagaacca ggacaatatt ttgcgcttct atctcaagga actaaccgtg      360
451 ttcgacgtag gcgacggttt cgtgaccaga gaacaactgc tgaaactgcg cgtcagcgat      420
453 gggaggctcc tctaccaact gacgttcgac gaagccctgg acctggtagc atcgccggaa      480
455 ggtaaagaat ttgccaggga cattcacgtg ttacgacgg aggtttcaga cgacgccaac      540
457 gcggtttcgg tgttcgacga cgacttaggt gaggacggcg taggcgagga gatccatacc      600
459 gtgcaagaag gaatgcagaa agtaccggag caactgctgc gtgcatttgg aaacagttcc      660

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VERIFICATION SUMMARY

DATE: 06/24/2005

PATENT APPLICATION: US/10/501,098

TIME: 11:27:05

Input Set : A:\4121-169.ST25.txt

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date